

Two Different Mutations in Codon 97 of the β -Globin Gene Cause Hb Malmö in Sweden

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An abnormal hemoglobin with increased oxygen affinity, Hb Malmö [$\alpha_2\beta_2$ 97(FG4)His→Gln], was found to cause erythrocytosis in two apparently unrelated Swedish families. Direct nucleotide sequencing of amplified DNA demonstrated a CAC→CAA substitution in one family and a CAC→CAG substitution in the other. Both mutations resulted in a His→Gln substitution in codon 97. This finding prompted us to examine the possible point mutations underlying the different hemoglobin variants reported in the literature.

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INTRODUCTION

Hb Malmö [$\alpha_2\beta_2$ 97(FG4)His→Gln] is an abnormal hemoglobin causing familial erythrocytosis which was described in 1970 [1] in a family (family A) living in southern Sweden. Soon afterwards it was found in a family in the US which had no obvious relation with the Swedish family, and Hb Malmö was then pointed out as the first erythrocytosis-producing hemoglobinopathy found in two apparently unrelated kindreds [2]. Later Hb Malmö was also found in a Sicilian family where the propositus was a compound heterozygote for Hb Malmö and β^0 -thalassemia [3]. From the proband's appearance (blond hair and blue eyes) a relation to the initial Swedish finding was assumed [3].

After the initial finding in four generations of family A, no additional cases of Hb Malmö were discovered in Sweden until 1993. Then a sample from a young man with erythrocytosis was subjected to hemoglobin investigation. Routine electrofocusing demonstrated an abnormal fraction and sequencing of the coding parts of the β -globin gene revealed a substitution CAC→CAG at codon 97, thus corresponding to Hb Malmö. Nucleotide sequencing of amplified material obtained from frozen hemolysates from family A did, however, clearly demonstrate a CAC→CAA substitution. This indicates that in Sweden, Hb Malmö originates from two separate mutations.

MATERIALS AND METHODS

Hematological data were obtained with local routine methods. Quantification of Hb F [4] and Hb A₂ [5] was made by ion-exchange high performance liquid chromatography (HPLC). Electrofocusing was routinely performed according to a slight modification [5] of the method originally published for separating Hb Malmö from Hb A [6].

DNA was extracted [7] from fresh EDTA blood (family B) or from a 23-year-old sample of hemolyzed red cells (family A). The latter was originally obtained by hemolysing washed red blood cells with distilled water, extracting with 0.1 volume carbon tetrachloride and adjusting the water phase to 0.1 M NaH₂PO₄, 10 mM KCN, 0.05 mM EDTA pH 7.0 prior to storage at -70°C . Amplification, purification of the amplified material, and nucleotide sequencing followed routine procedures [8] except that 16

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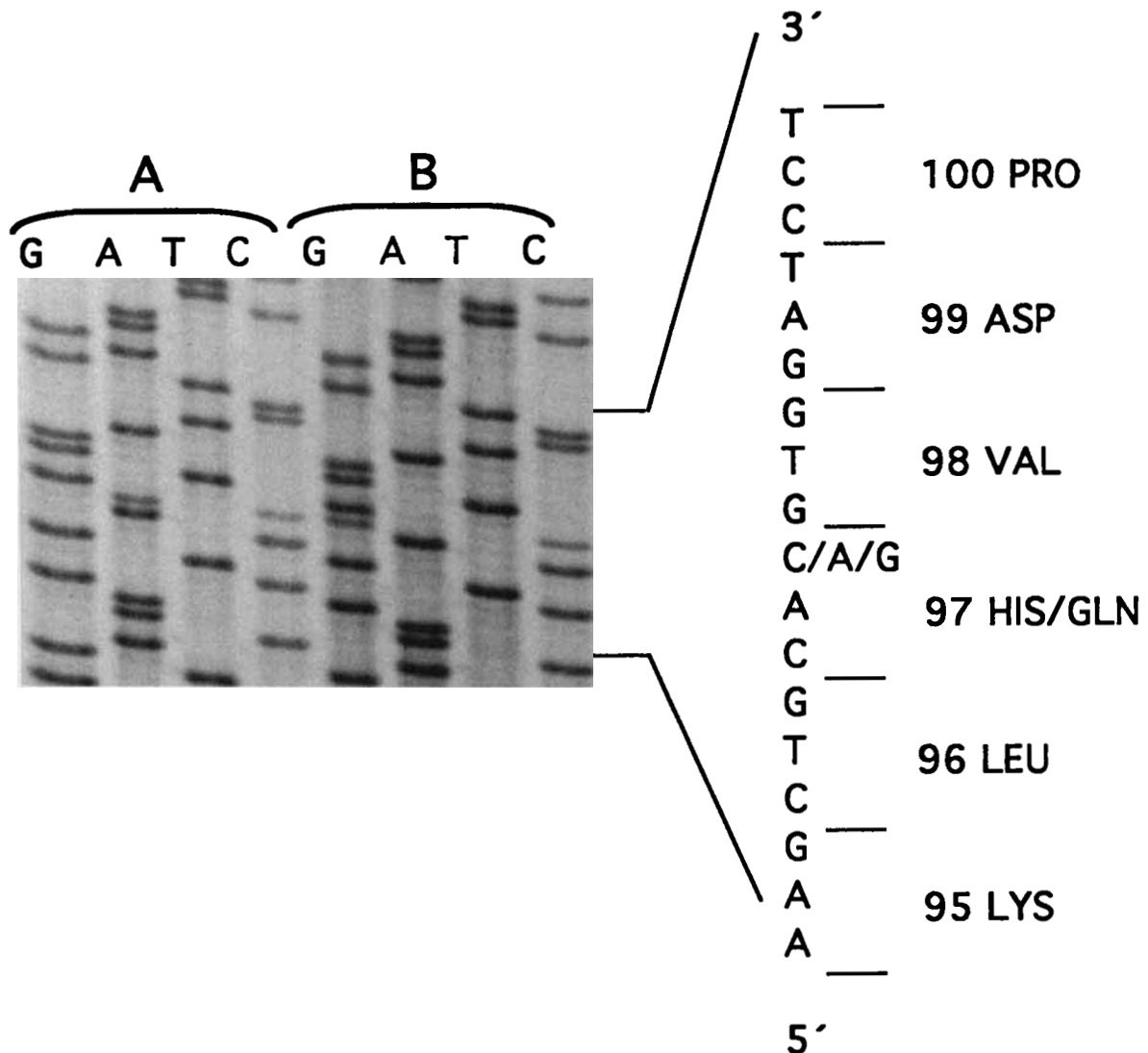


Fig. 1. Sequence analysis of amplified β -globin DNA from members of two different families, both showing heterozygosity for Hb Malmö. In family A the codon 97 mutation CAC \rightarrow CAA was found, while in family B the mutation was CAC \rightarrow CAG. Both mutations will result in a His \rightarrow Gln substitution. The sequencing primer corresponded to codon 62 to 68.

μ g bovine serum albumin was included in the 100 μ L incubations used for amplifying DNA from family A. Six different polymorphic restriction enzyme sites in the β -globin cluster were amplified and cleaved to give an indication of haplotype pattern [9].

RESULTS

The proband in family B was a 26-year-old male with hemoglobin 200 g/L, hematocrit 59%, WBC 6.4×10^9 /L and PLT 186×10^9 /L. HbA₂ was 2.8% and HbF was not detectable. Electrofocusing demonstrated a distinct abnormal anodal fraction. No major variant fraction was separated at the HPLCs used for HbA₂ or HbF quantita-

tions but the HbF chromatogram [4] demonstrated a duplicated HbA_{1c} peak. The fraction eluting somewhat prior to the normal HbA_{1c} fraction from the cation exchange resin contained 1.3% of the total hemoglobin content and probably comprised the N-terminally glycosylated form of the variant hemoglobin, while the normal HbA_{1c} fraction contained 2.1% of total hemoglobin.

Nucleotide sequencing demonstrated a substitution CAC \rightarrow CAG at codon 97 in the β -globin gene (Fig. 1), thus corresponding to Hb Malmö. Family B lived 800 km from family A and had no known relatives in the southern part of Sweden where family A lived. Since it was realized that two different nucleotide substitutions might cause the same hemoglobin variant, we also tried

TABLE I. β -Globin Variants Described in the Literature, Where More Than One Nucleotide Substitution Could Cause the Same Phenotype

Normal			Variant		
Position	Code	Amino acid	Possible codes	Amino acid	Name
β 2	CAC	His	CAG/CAA	Gln	Hb Okayama
β 15	TGG	Arg	AGG/CGG	Arg	Hb Belfast
β 17	AAG	Lys	ATT/AAC	Asn	Hb J-Amiens
β 19	AAC	Asn	AAG/AAA	Lys	Hb D-Ouled Rabah
β 30	AGG	Arg	AGT/AGC	Ser	Hb Tacoma
β 37	TGG	Trp	AGG/CGG	Arg	Hb Rothschild
β 40	AGG	Arg	AGT/AGC	Ser	Hb Austin
β 42	TTT	Phe	CTT/TTG/TTA	Leu	Hb Louisville
β 46	GGG	Gly	AGG/CGG	Arg	Hb Gainesville-GA
β 57	AAC	Asn	AAG/AAA	Lys	Hb G-Ferrara
β 59	AAG	Lys	AAT/AAC	Asn	Hb J-Lome
β 60	GTG	Val	TTG/CTG	Leu	Hb Yatsushiro
β 61	AAG	Lys	AAT/AAC	Asn	Hb Hikari
β 65	AAG	Lys	AAT/AAC	Asn	Hb J-Sicilia
β 80	AAC	Asn	AAG/AAA	Lys	Hb G-Szuhu
β 82	AAG	Lys	AAT/AAC	Asn (\rightarrow Asp)	Hb Providence
β 90	GAG	Glu	GAT/GAC	Asp	Hb Pierre-Bénite
β 92	CAC	His	CAG/CAA	Gln	Hb St. Etienne
β 95	AAG	Lys	AAT/AAC	Asn	Hb Detroit
β 97	CAC	His	CAG/CAA	Gln	Hb Malmö
β 99	GAT	Asp	GAA/GAG	Glu	Hb Coimbra
β 101	GAG	Glu	GAT/GAC	Asp	Hb Potomac
β 102	AAC	Asn	AAG/AAA	Lys	Hb Richmond
β 103	TTC	Phe	CTC/TTG/TTA	Leu	Hb Heathrow
β 104	AGG	Arg	AGT/AGC	Ser	Hb Camperdown
β 108	AAC	Asn	AAG/AAA	Lys	Hb Presbyterian
β 109	GTG	Val	TTG/CTG	Leu	Hb Johnstown
β 116	CAT	His	CAG/CAA	Gln	Hb Hafnia
β 120	AAA	Lys	AAT/AAC	Asn	Hb Riyadh
β 132	AAA	Lys	AAT/AAC	Asn	Hb Yamagata
β 133	GTG	Val	TTG/CTG	Leu	Hb Extremadura
β 139	AAT	Asn	AAG/AAA	Lys	Hb Hinsdale
β 143	CAC	His	CAG/CAA	Gln	Hb Little Rock
β 145	TAT	Tyr	TAG/TAA	Term.	Hb McKees Rock

to elucidate the underlying nucleotide substitution in the original family A. Unfortunately, no members of this family could be reached for sampling, so DNA had to be extracted from an old hemolysate which was kept frozen in the laboratory as a potential reference sample for electrofocusing. DNA was successfully obtained from this sample and the other possible substitution corresponding to Hb Malmö, CAC \rightarrow CAA (Fig. 1), turned out to be present in family A. Samples from both families were sequenced twice on two separate occasions, each using pooled material from two freshly performed separate amplifications.

The proband in family B was homozygous for a haplotype resembling haplotype I or V, both haplotypes being compatible with the findings in the sole representative of family A that could be investigated. In family B, the variant was present only in the proband and not in his mother or sister. The deceased father, a non-smoker, was treated for hypertension detected at the age of 38 and

had a myocardial infarct at the age of 43. Three months later, he was hospitalized for treatment of transitory brain stem ischemia and had a hemoglobin concentration of 149 g/L and hematocrit of 42%. He died at the age of 49, presumably of a myocardial infarct. No other relatives of the father were available for investigation.

Looking through the other β -globin variants reported to the International Hemoglobin Information Center [10] revealed that 34 of the 316 β -globin variants assumed to be due to single amino acid substitutions could be caused by more than one type of point mutation at the DNA level (Table I). With the exception Hb Malmö, we only have experience with two of these variants. Hb Okayama has been found in Sweden in two seemingly unrelated patients, both of them showing the codon 2 CAC \rightarrow CAA mutation. One of the carriers was an ethnic Swede while the other had relations to Austria and Germany. In addition, Hb Tacoma due to the codon 30 AGG \rightarrow AGT substitution has been found in Sweden [6] in several members

TABLE II. β - and α -Globin Variants Where Reported Amino Acid Substitutions Are Not Compatible With Single Point Nucleotide Substitutions

Variant	Position	Codon	Amino acid replacement	Assumed codon in variant	Reference
Hb Edmonton	β 50	ACT	Thr→Lys	AAA; AAG	[15]
Hb Bristol	β 67	GTG	Val→Asp	GAT; GAC	[16]
Hb Beckman	β 135	GCG	Ala→Glu	GAA; GAG	[17]
Hb J-Kurosh	α 19	GCG	Ala→Asp	GAT; GAC	[18]

of three not obviously related families. However, all these families are of Finnish descent, so they are likely to share a common origin with other published cases carrying this variant [11].

The study of the list of reported β -globin variants also indicated that three of the β -globin and one of the α -globin variants reported were not compatible with single transitions or transversions in the normal globin gene sequence (Table II).

DISCUSSION

It is well known that the same hemoglobin variant may occur independently in families of widely different ethnic origin. In Sweden this has been exemplified by the finding of Hb K-Ibadan and Hb Fukuyama in ethnic Swedes [5]. Sometimes de novo mutations are observed, most commonly when the mutations result in an unstable β -globin variant, e.g., Hb Köln [12] or Hb Altdorf [13].

That different nucleotide substitutions might cause the same hemoglobin variant was recently demonstrated by Molchanova et al. [14] who described two different mutations causing Hb G-Philadelphia. These mutations occur on either the normal α 2-globin gene or on the hybrid α 2 α 1-gene found on $-\alpha^{3,7}$ chromosomes. We now report the first example of a β -globin variant being caused by two different mutations. Furthermore, the two mutations at codon 97, CAC→CAA and CAC→CAG, both presenting as Hb Malmö, occurred in the same ethnic group. This finding reminds us that the sole fact that a hemoglobin variant is found in two families in the same population does not entitle us to regard the families as related.

For those hemoglobin variants, of which already more than 30 are described, where more than one underlying mutation is possible, reports containing not only the amino acid substitution but also the underlying mutation are desired. As exemplified in the present report, even hemolyzed red cells that have been stored frozen for many years can be used as the source of DNA for amplifications. Hence information about nucleotide substitutions could be obtained on several variants already described.

The finding in the literature of three β - and one α -globin variant that are not compatible with single point nucleotide substitutions is intriguing. The possible rea-

sons for this discrepancy are, however, beyond the scope of this report.

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